

SEQUENCE LISTING

<110> Martin Richard
 Flatt Brenton Todd
 Kahl Jeffrey Dean
 Wang Tie-Lin

<120> HETEROCYCLIC MODULATORS OF NUCLEAR RECEPTORS

<130> 38205-3001B

<140> Unassigned
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<150> 10/329,668
 <151> 2002-12-20

<150> 60/342,720
 <151> 2001-12-21

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<170> FastSEQ for Windows Version 4.0

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	Ala Pro Val Pro Asp Ile Pro Pro Asp Ser Ala Val Glu Leu Trp Lys	
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	cca ggc gca cag gat gca agc agc cag gcc cag gga ggc agc agc tgc	149
	Pro Gly Ala Gln Asp Ala Ser Ser Gln Ala Gln Gly Gly Ser Ser Cys	
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	atc ctc aga gag gaa gcc agg atc ccc cac tct gct ggg ggt act gca	197
	Ile Leu Arg Glu Ala Arg Met Pro His Ser Ala Gly Gly Thr Ala	
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	ggg gtg ggg ctg gag gct gca gag ccc aca gcc ctg ctc acc agg gca	245
	Gly Val Gly Leu Glu Ala Ala Glu Pro Thr Ala Leu Leu Thr Arg Ala	
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	gag ccc cct tca gaa ccc aca gag atc cgt cca caa aag cgg aaa aag	293
	Glu Pro Pro Ser Glu Pro Thr Glu Ile Arg Pro Gln Lys Arg Lys Lys	
	75	80
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	ggg cca gcc ccc aaa atg ctg ggg aac gag cta tgc agc gtg tgt ggg	341
	Gly Pro Ala Pro Lys Met Leu Gly Asn Glu Leu Cys Ser Val Cys Gly	

90	95	100	
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aag gga ttc ttc cgc cgc agc gtc atc aag gga gcg cac tac atc tgc Lys Gly Phe Phe Arg Arg Ser Val Ile Lys Gly Ala His Tyr Ile Cys 120 125 130			437
cac agt ggc ggc cac tgc ccc atg gac acc tac atg cgt cgc aag tgc His Ser Gly Gly His Cys Pro Met Asp Thr Tyr Met Arg Arg Lys Cys 135 140 145 150			485
cag gag tgt cgg ctt cgc aaa tgc cgt cag gct ggc atg cg ^g gag gag Gln Glu Cys Arg Leu Arg Lys Cys Arg Gln Ala Gly Met Arg Glu Glu 155 160 165			533
tgt gtc ctg tca gaa gaa cag atc cgc ctg aag aaa ctg aag cg ^g caa Cys Val Leu Ser Glu Glu Gln Ile Arg Leu Lys Lys Leu Lys Arg Gln 170 175 180			581
gag gag gaa cag gct cat gcc aca tcc ttg ccc ccc agg cgt tcc tca Glu Glu Glu Gln Ala His Ala Thr Ser Leu Pro Pro Arg Arg Ser Ser 185 190 195			629
ccc ccc caa atc ctg ccc cag ctc agc ccg gaa caa ctg ggc atg atc Pro Pro Gln Ile Leu Pro Gln Leu Ser Pro Glu Gln Leu Gly Met Ile 200 205 210			677
gag aag ctc gtc gct gcc cag caa cag tgt aac cgg cgc tcc ttt tct Glu Lys Leu Val Ala Ala Gln Gln Gln Cys Asn Arg Arg Ser Phe Ser 215 220 225 230			725
gac cgg ctt cga gtc acg cct tgg ccc atg gca cca gat ccc cat agc Asp Arg Leu Arg Val Thr Pro Trp Pro Met Ala Pro Asp Pro His Ser 235 240 245			773
cgg gag gcc cgt cag cag cgc ttt gcc cac ttc act gag ctg gcc atc Arg Glu Ala Arg Gln Gln Arg Phe Ala His Phe Thr Glu Leu Ala Ile 250 255 260			821
gtc tct gtg cag gag ata gtt gac ttt gct aaa cag cta ccc ggc ttc Val Ser Val Gln Glu Ile Val Asp Phe Ala Lys Gln Leu Pro Gly Phe 265 270 275			869
ctg cag ctc agc cgg gag gac cag att gcc ctg ctg aag acc tct gcg Leu Gln Leu Ser Arg Glu Asp Gln Ile Ala Leu Leu Lys Thr Ser Ala 280 285 290			917
atc gag gtg atg ctt ctg gag aca tct cgg agg tac aac ccc ggg agt Ile Glu Val Met Leu Leu Glu Thr Ser Arg Arg Tyr Asn Pro Gly Ser 295 300 305 310			965
gag agt atc acc ttc ctc aag gat ttc agt tat aac cgg gaa gac ttt Glu Ser Ile Thr Phe Leu Lys Asp Phe Ser Tyr Asn Arg Glu Asp Phe 315 320 325			1013
gcc aaa gca ggg ctg caa gtg gaa ttc atc aac ccc atc ttc gag ttc Ala Lys Ala Gly Leu Gln Val Glu Phe Ile Asn Pro Ile Phe Glu Phe 330 335 340			1061
tcc agg gcc atg aat gag ctg caa ctc aat gat gcc gag ttt gcc ttg Ser Arg Ala Met Asn Glu Leu Gln Leu Asn Asp Ala Glu Phe Ala Leu 345 350 355			1109
ctc att gct atc agc atc ttc tct gca gac cgg ccc aac gtg cag gac			1157

Leu Ile Ala Ile Ser Ile Phe Ser Ala Asp Arg Pro Asn Val Gln Asp			
360	365	370	
cag ctc cag gtg gag agg ctg cag cac aca tat gtg gaa gcc ctg cat			1205
Gln Leu Gln Val Glu Arg Leu Gln His Thr Tyr Val Glu Ala Leu His			
375	380	385	390
gcc tac gtc tcc atc cac cat ccc cat gac cga ctg atg ttc cca cgg			1253
Ala Tyr Val Ser Ile His His Pro His Asp Arg Leu Met Phe Pro Arg			
395	400	405	
atg cta atg aaa ctg gtg agc ctc cg acc ctg agc agc gtc cac tca			1301
Met Leu Met Lys Leu Val Ser Leu Arg Thr Leu Ser Ser Val His Ser			
410	415	420	
gag caa gtg ttt gca ctg cgt ctg cag gac aaa aag ctc cca ccg ctg			1349
Glu Gln Val Phe Ala Leu Arg Leu Gln Asp Lys Lys Leu Pro Pro Leu			
425	430	435	
ctc tct gag atc tgg gat gtg cac gaa tga ctgttctgtc cccatatttt			1399
Leu Ser Glu Ile Trp Asp Val His Glu *			
440	445		
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Gln Gly Gly Ser Ser Cys Ile Leu Arg Glu Glu Ala Arg Met Pro His			
35 40 45			
Ser Ala Gly Gly Thr Ala Gly Val Gly Leu Glu Ala Ala Glu Pro Thr			
50 55 60			
Ala Leu Leu Thr Arg Ala Glu Pro Pro Ser Glu Pro Thr Glu Ile Arg			
65 70 75 80			
Pro Gln Lys Arg Lys Lys Gly Pro Ala Pro Lys Met Leu Gly Asn Glu			
85 90 95			
Leu Cys Ser Val Cys Gly Asp Lys Ala Ser Gly Phe His Tyr Asn Val			
100 105 110			
Leu Ser Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Val Ile Lys			
115 120 125			
Gly Ala His Tyr Ile Cys His Ser Gly Gly His Cys Pro Met Asp Thr			
130 135 140			
Tyr Met Arg Arg Lys Cys Gln Glu Cys Arg Leu Arg Lys Cys Arg Gln			
145 150 155 160			
Ala Gly Met Arg Glu Glu Cys Val Leu Ser Glu Glu Gln Ile Arg Leu			
165 170 175			
Lys Lys Leu Lys Arg Gln Glu Glu Gln Ala His Ala Thr Ser Leu			
180 185 190			
Pro Pro Arg Arg Ser Ser Pro Pro Gln Ile Leu Pro Gln Leu Ser Pro			
195 200 205			
Glu Gln Leu Gly Met Ile Glu Lys Leu Val Ala Ala Gln Gln Gln Cys			
210 215 220			
Asn Arg Arg Ser Phe Ser Asp Arg Leu Arg Val Thr Pro Trp Pro Met			
225 230 235 240			
Ala Pro Asp Pro His Ser Arg Glu Ala Arg Gln Gln Arg Phe Ala His			
245 250 255			
Phe Thr Glu Leu Ala Ile Val Ser Val Gln Glu Ile Val Asp Phe Ala			
260 265 270			

Lys Gln Leu Pro Gly Phe Leu Gln Leu Ser Arg Glu Asp Gln Ile Ala
 275 280 285
 Leu Leu Lys Thr Ser Ala Ile Glu Val Met Leu Leu Glu Thr Ser Arg
 290 295 300
 Arg Tyr Asn Pro Gly Ser Glu Ser Ile Thr Phe Leu Lys Asp Phe Ser
 305 310 315 320
 Tyr Asn Arg Glu Asp Phe Ala Lys Ala Gly Leu Gln Val Glu Phe Ile
 325 330 335
 Asn Pro Ile Phe Glu Phe Ser Arg Ala Met Asn Glu Leu Gln Leu Asn
 340 345 350
 Asp Ala Glu Phe Ala Leu Leu Ile Ala Ile Ser Ile Phe Ser Ala Asp
 355 360 365
 Arg Pro Asn Val Gln Asp Gln Leu Gln Val Glu Arg Leu Gln His Thr
 370 375 380
 Tyr Val Glu Ala Leu His Ala Tyr Val Ser Ile His His Pro His Asp
 385 390 395 400
 Arg Leu Met Phe Pro Arg Met Leu Met Lys Leu Val Ser Leu Arg Thr
 405 410 415
 Leu Ser Ser Val His Ser Glu Gln Val Phe Ala Leu Arg Leu Gln Asp
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 Lys Lys Leu Pro Pro Leu Leu Ser Glu Ile Trp Asp Val His Glu
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<220>
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 <222> (56) ... (1438)

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 <309> 2002-08-01

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 Ser Ser Pro Thr Ser Ser Leu Asp Thr Pro Leu Pro Gly Asn Gly
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 ccc cct cag cct ggc gcc cct tct tct tca ccc act gta aag gag gag 154
 Pro Pro Gln Pro Gly Ala Pro Ser Ser Pro Thr Val Lys Glu Glu
 20 25 30
 ggt ccg gag ccg tgg ccc ggg ggt ccg gac cct gat gtc cca ggc act 202
 Gly Pro Glu Pro Trp Pro Gly Gly Pro Asp Pro Asp Val Pro Gly Thr
 35 40 45
 gat gag gcc agc tca gcc tgc agc aca gac tgg gtc atc cca gat ccc 250
 Asp Glu Ala Ser Ser Ala Cys Ser Thr Asp Trp Val Ile Pro Asp Pro
 50 55 60 65
 gaa gag gaa cca gag cgc aag cga aag aag ggc cca gcc ccg aag atg 298
 Glu Glu Glu Pro Glu Arg Lys Arg Lys Lys Gly Pro Ala Pro Lys Met
 70 75 80
 ctg ggc cac gag ctt tgc cgt gtc tgt ggg gac aag gcc tcc ggc ttc 346
 Leu Gly His Glu Leu Cys Arg Val Cys Gly Asp Lys Ala Ser Gly Phe
 85 90 95
 cac tac aac gtg ctc agc tgc gaa ggc tgc aag ggc ttc ttc cgg cgc 394

His	Tyr	Asn	Val	Leu	Ser	Cys	Glu	Gly	Cys	Lys	Gly	Phe	Phe	Arg	Arg		
100							105					110					
agt	gtg	gtc	cgt	ggt	ggg	gcc	agg	cgc	tat	gcc	tgc	cgg	ggt	ggc	gga	442	
Ser	Val	Val	Arg	Gly	Gly	Ala	Arg	Arg	Tyr	Ala	Cys	Arg	Gly	Gly	Gly		
115						120					125						
acc	tgc	cag	atg	gac	gct	ttc	atg	cg	cg	aag	tgc	cag	cag	tgc	cg	490	
Thr	Cys	Gln	Met	Asp	Ala	Phe	Met	Arg	Arg	Lys	Cys	Gln	Gln	Cys	Arg		
130						135					140				145		
ctg	cgc	aag	tgc	aag	gag	gca	ggg	atg	agg	gag	cag	tgc	gtc	ctt	tct	538	
Leu	Arg	Lys	Cys	Lys	Glu	Ala	Gly	Met	Arg	Glu	Gln	Cys	Val	Leu	Ser		
						150				155				160			
gaa	gaa	cag	atc	cg	aag	aag	aag	att	cg	aaa	cag	cag	cag	gag	tca	586	
Glu	Glu	Gln	Ile	Arg	Lys	Lys	Lys	Ile	Arg	Lys	Gln	Gln	Gln	Glu	Ser		
						165				170				175			
cag	tca	cag	tcg	cag	tca	cct	gtg	ggg	ccg	cag	ggc	agc	agc	agc	tca	634	
Gln	Ser	Gln	Ser	Gln	Ser	Pro	Val	Gly	Pro	Gln	Gly	Ser	Ser	Ser	Ser		
						180			185			190					
gcc	tct	ggg	cct	ggg	gct	tcc	cct	gg	tct	gag	gca	ggc	agc	cag		682	
Ala	Ser	Gly	Pro	Gly	Ala	Ser	Pro	Gly	Gly	Ser	Glu	Ala	Gly	Ser	Gln		
						195			200			205					
ggc	tcc	ggg	gaa	ggc	gag	gg	gtc	cag	cta	aca	g	g	g	g		730	
Gly	Ser	Gly	Glu	Gly	Gly	Gly	Val	Gln	Leu	Thr	Ala	Ala	Gln	Glu	Leu		
						210			215			220			225		
atg	atc	cag	cag	ttg	gtg	g	cc	caa	ctg	cag	tgc	aac	aaa	cgc	tcc	778	
Met	Ile	Gln	Gln	Leu	Val	Ala	Ala	Gln	Leu	Gln	Cys	Asn	Lys	Arg	Ser		
						230			235			240					
tcc	tcc	gac	cag	ccc	aaa	gtc	ac	ccc	tgg	ccc	ctg	ggc	gca	gac	ccc	826	
Phe	Ser	Asp	Gln	Pro	Lys	Val	Thr	Pro	Trp	Pro	Leu	Gly	Ala	Asp	Pro		
						245			250			255					
cag	tcc	cga	gat	gcc	cgc	cag	caa	cgc	ttt	gcc	cac	ttc	acg	gag	ctg	874	
Gln	Ser	Arg	Asp	Ala	Arg	Gln	Gln	Arg	Phe	Ala	His	Phe	Thr	Glu	Leu		
						260			265			270					
gcc	atc	atc	tca	gtc	cag	gag	atc	gtg	gac	ttc	gct	aag	caa	gtg	cct	922	
Ala	Ile	Ile	Ser	Val	Gln	Glu	Ile	Val	Asp	Phe	Ala	Lys	Gln	Val	Pro		
						275			280			285					
gg	t	tc	ct	cg	ct	gg	cg	g	g	ac	atc	g	cc	ct	ct	970	
Gly	Phe	Leu	Gln	Leu	Gly	Arg	Glu	Asp	Gln	Ile	Ala	Leu	Leu	Lys	Ala		
						290			295			300			305		
tcc	act	atc	gag	atc	atg	ct	ta	gag	aca	g	cc	agg	cgc	ta	ac	1018	
Ser	Thr	Ile	Glu	Ile	Met	Leu	Leu	Glu	Thr	Ala	Arg	Arg	Tyr	Asn	His		
						310			315			320					
gag	aca	gag	tgt	atc	acc	ttc	ttg	aag	gac	ttc	acc	ta	c	ag	gac	1066	
Glu	Thr	Glu	Cys	Ile	Thr	Phe	Leu	Lys	Asp	Phe	Thr	Tyr	Ser	Lys	Asp		
						325			330			335					
gac	t	tc	cac	cgt	gca	gg	ct	cg	tg	gag	ttc	atc	aa	cc	atc	ttc	1114
Asp	Phe	His	Arg	Ala	Gly	Leu	Gln	Val	Glu	Phe	Ile	Asn	Pro	Ile	Phe		
						340			345			350					
gag	t	tc	cg	gg	gc	at	cg	cg	ct	gg	ct	g	ac	g	ct	1162	
Glu	Phe	Ser	Arg	Ala	Met	Arg	Arg	Leu	Gly	Leu	Asp	Asp	Ala	Glu	Tyr		
						355			360			365					

gcc ctg ctc atc gcc atc aac atc ttc tcg gcc gac cgg ccc aac gtg	1210
Ala Leu Leu Ile Ala Ile Asn Ile Phe Ser Ala Asp Arg Pro Asn Val	
370 375 380 385	
cag gag ccg ggc cgc gtg gag gcg ttg cag cag ccc tac gtg gag gcg	1258
Gln Glu Pro Gly Arg Val Glu Ala Leu Gln Gln Pro Tyr Val Glu Ala	
390 395 400	
ctg ctg tcc tac acg cgc atc aag agg ccg cag gac cag ctg cgc ttc	1306
Leu Leu Ser Tyr Thr Arg Ile Lys Arg Pro Gln Asp Gln Leu Arg Phe	
405 410 415	
ccg cgc atg ctc atg aag ctg gtg agc ctg cgc acg ctg agc tct gtg	1354
Pro Arg Met Leu Met Lys Leu Val Ser Leu Arg Thr Leu Ser Ser Val	
420 425 430	
cac tcg gag cag gtc ttc gcc ttg cgg ctc cag gac aag aag ctg ccg	1402
His Ser Glu Gln Val Phe Ala Leu Arg Leu Gln Asp Lys Lys Leu Pro	
435 440 445	
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Pro Leu Leu Ser Glu Ile Trp Asp Val His Glu *	
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ggataagccc cagtccaggt ccaggaggt ccctccctgc ccagcgagtc ttccagaagg	1628
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acacctaag cccagcacgc agtgcacctt gaacagaggg aggggaggac ccatggctct	1748
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aaaacag	1815

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<212> PRT
<213> Homo Sapien

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35 40 45	
Thr Asp Glu Ala Ser Ser Ala Cys Ser Thr Asp Trp Val Ile Pro Asp	
50 55 60	
Pro Glu Glu Glu Pro Glu Arg Lys Arg Lys Lys Gly Pro Ala Pro Lys	
65 70 75 80	
Met Leu Gly His Glu Leu Cys Arg Val Cys Gly Asp Lys Ala Ser Gly	
85 90 95	
Phe His Tyr Asn Val Leu Ser Cys Glu Gly Cys Lys Gly Phe Phe Arg	
100 105 110	
Arg Ser Val Val Arg Gly Gly Ala Arg Arg Tyr Ala Cys Arg Gly Gly	
115 120 125	
Gly Thr Cys Gln Met Asp Ala Phe Met Arg Arg Lys Cys Gln Gln Cys	
130 135 140	
Arg Leu Arg Lys Cys Lys Glu Ala Gly Met Arg Glu Gln Cys Val Leu	
145 150 155 160	
Ser Glu Glu Gln Ile Arg Lys Lys Ile Arg Lys Gln Gln Gln Glu	
165 170 175	
Ser Gln Ser Gln Ser Gln Ser Pro Val Gly Pro Gln Gly Ser Ser Ser	
180 185 190	
Ser Ala Ser Gly Pro Gly Ala Ser Pro Gly Gly Ser Glu Ala Gly Ser	
195 200 205	
Gln Gly Ser Gly Glu Gly Glu Val Gln Leu Thr Ala Ala Gln Glu	
210 215 220	
Leu Met Ile Gln Gln Leu Val Ala Ala Gln Leu Gln Cys Asn Lys Arg	

225	230	235	240
Ser Phe Ser Asp Gln Pro Lys Val Thr Pro Trp Pro Leu Gly Ala Asp			
245	250	255	
Pro Gln Ser Arg Asp Ala Arg Gln Gln Arg Phe Ala His Phe Thr Glu			
260	265	270	
Leu Ala Ile Ile Ser Val Gln Glu Ile Val Asp Phe Ala Lys Gln Val			
275	280	285	
Pro Gly Phe Leu Gln Leu Gly Arg Glu Asp Gln Ile Ala Leu Leu Lys			
290	295	300	
Ala Ser Thr Ile Glu Ile Met Leu Leu Glu Thr Ala Arg Arg Tyr Asn			
305	310	315	320
His Glu Thr Glu Cys Ile Thr Phe Leu Lys Asp Phe Thr Tyr Ser Lys			
325	330	335	
Asp Asp Phe His Arg Ala Gly Leu Gln Val Glu Phe Ile Asn Pro Ile			
340	345	350	
Phe Glu Phe Ser Arg Ala Met Arg Arg Leu Gly Leu Asp Asp Ala Glu			
355	360	365	
Tyr Ala Leu Leu Ile Ala Ile Asn Ile Phe Ser Ala Asp Arg Pro Asn			
370	375	380	
Val Gln Glu Pro Gly Arg Val Glu Ala Leu Gln Gln Pro Tyr Val Glu			
385	390	395	400
Ala Leu Leu Ser Tyr Thr Arg Ile Lys Arg Pro Gln Asp Gln Leu Arg			
405	410	415	
Phe Pro Arg Met Leu Met Lys Leu Val Ser Leu Arg Thr Leu Ser Ser			
420	425	430	
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<309> 1995-06-21

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caccatcccc gaagcacatt ctcgagttga aaagttggag tgggtttcga a atg aat 177
Met Asn
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ctg att ggg ccc tcc cat tta caa gcc acg gac gag ttt gct ctt tct 225
Leu Ile Gly Pro Ser His Leu Gln Ala Thr Asp Glu Phe Ala Leu Ser
5 10 15

gaa aac tta ttt gga gtg cta aca gag cac gcg gca ggt cct ctg ggg 273
Glu Asn Leu Phe Gly Val Leu Thr Glu His Ala Ala Gly Pro Leu Gly
20 25 30

cag aat ctg gac ttg gaa tcg tac tcc cca tac aac aat gtg cag ttt 321
Gln Asn Leu Asp Leu Glu Ser Tyr Ser Pro Tyr Asn Asn Val Gln Phe
35 40 45 50

cct caa gtt cag cca cag atc tcc tcc tcg tcc tat tat tcc aac ctg 369
Pro Gln Val Gln Pro Gln Ile Ser Ser Ser Tyr Tyr Ser Asn Leu
55 60 65

ggt ttc tac ccg caa caa ccg gaa gac tgg tac tct cct gga ctc tat		417
Gly Phe Tyr Pro Gln Gln Pro Glu Asp Trp Tyr Ser Pro Gly Leu Tyr		
70	75	80
gaa ctc agg cga atg ccc act gag agt gtg tac cag gga gag act gag		465
Glu Leu Arg Arg Met Pro Thr Glu Ser Val Tyr Gln Gly Glu Thr Glu		
85	90	95
gta tcc gag atg cct gtg aca aag aag ccg cga atg gcc gcc tca tcg		513
Val Ser Glu Met Pro Val Thr Lys Lys Pro Arg Met Ala Ala Ser Ser		
100	105	110
gcg gga aga ata aaa ggg gat gag ctg tgt gtg gtc tgc gga gac agg		561
Ala Gly Arg Ile Lys Gly Asp Glu Leu Cys Val Val Cys Gly Asp Arg		
115	120	125
130		
gcc tct ggg tac cat tac aac gcg ctc acc tgc gag ggc tgc aaa ggt		609
Ala Ser Gly Tyr His Tyr Asn Ala Leu Thr Cys Glu Gly Cys Lys Gly		
135	140	145
ttc ttc cga aga agc atc acc aaa aac gcc gtg tac aag tgt aag aac		657
Phe Phe Arg Arg Ser Ile Thr Lys Asn Ala Val Tyr Lys Cys Lys Asn		
150	155	160
ggg ggc aac tgc gtg atg gat atg tac atg cgt cgg aag tgc cag gat		705
Gly Gly Asn Cys Val Met Asp Met Tyr Met Arg Arg Lys Cys Gln Asp		
165	170	175
tgc cgg cta agg aag tgc aga gag atg gga atg ttg gct gaa tgt ttg		753
Cys Arg Leu Arg Lys Cys Arg Glu Met Gly Met Leu Ala Glu Cys Leu		
180	185	190
tta act gaa att cag tgt aaa tct aaa cgg cta agg aaa aat gtg aag		801
Leu Thr Glu Ile Gln Cys Lys Ser Lys Arg Leu Arg Lys Asn Val Lys		
195	200	205
210		
cag cat gcg gat cag aca gtg aat gag gac agc gaa ggg cgt gac ttg		849
Gln His Ala Asp Gln Thr Val Asn Glu Asp Ser Glu Gly Arg Asp Leu		
215	220	225
cgg caa gtg acc tcc acg acc aag cta tgc agg gag aaa act gaa ctc		897
Arg Gln Val Thr Ser Thr Lys Leu Cys Arg Glu Lys Thr Glu Leu		
230	235	240
act gta gac cag cag acc ctc ctg gat tat att atg gac tca tac agc		945
Thr Val Asp Gln Gln Thr Leu Leu Asp Tyr Ile Met Asp Ser Tyr Ser		
245	250	255
aaa cag aga atg cca cag gag atc aca aat aaa atc tta aaa gaa gaa		993
Lys Gln Arg Met Pro Gln Glu Ile Thr Asn Lys Ile Leu Lys Glu Glu		
260	265	270
ttt agt gca gaa gaa aat ttt ctc ata tta aca gaa atg gct acc agt		1041
Phe Ser Ala Glu Glu Asn Phe Leu Ile Leu Thr Glu Met Ala Thr Ser		
275	280	285
290		
cac gta cag att ctc gta gaa ttc aca aaa aga ctt cca ggg ttt cag		1089
His Val Gln Ile Leu Val Glu Phe Thr Lys Arg Leu Pro Gly Phe Gln		
295	300	305
aca ctg gac cac gaa gac cag att gct ttg ctc aaa ggg tcc gca gtc		1137
Thr Leu Asp His Glu Asp Gln Ile Ala Leu Leu Lys Gly Ser Ala Val		
310	315	320
gag gcc atg ttc ctt cgt tca gcg gag att ttc aat aag aaa ctt cct		1185
Glu Ala Met Phe Leu Arg Ser Ala Glu Ile Phe Asn Lys Lys Leu Pro		
325	330	335

gcc gga cac gca gac ctg ttg gaa gaa aga att cga aag agc ggc atc	1233
Ala Gly His Ala Asp Leu Leu Glu Glu Arg Ile Arg Lys Ser Gly Ile	
340 345 350	
tcc gat gag tac ata acc ccg atg ttt agt ttc tat aaa agt gtc ggg	1281
Ser Asp Glu Tyr Ile Thr Pro Met Phe Ser Phe Tyr Lys Ser Val Gly	
355 360 365 370	
gag ctg aaa atg acc cag gaa gag tac gct ctg ctc aca gca att gtc	1329
Glu Leu Lys Met Thr Gln Glu Glu Tyr Ala Leu Leu Thr Ala Ile Val	
375 380 385	
atc ctc tct cca gac aga caa tac ata aag gat aga gag gca gtg gag	1377
Ile Leu Ser Pro Asp Arg Gln Tyr Ile Lys Asp Arg Glu Ala Val Glu	
390 395 400	
aag ctt cag gag cct ctc gat gtc cta caa aaa ctc tgc aag atc	1425
Lys Leu Gln Glu Pro Leu Leu Asp Val Leu Gln Lys Leu Cys Lys Ile	
405 410 415	
tac cag ccc gag aac cct cag cat ttc gcc tgc ctc ctg ggt cgc ctg	1473
Tyr Gln Pro Glu Asn Pro Gln His Phe Ala Cys Leu Leu Gly Arg Leu	
420 425 430	
aca gaa ctc cgg aca ttc aac cat cac cac gct gag atg ctg atg tct	1521
Thr Glu Leu Arg Thr Phe Asn His His His Ala Glu Met Leu Met Ser	
435 440 445 450	
tgg agg gtg aat gac cac aag ttc acc ccg ctc ctc tgt gag atc tgg	1569
Trp Arg Val Asn Asp His Lys Phe Thr Pro Leu Leu Cys Glu Ile Trp	
455 460 465	
gat gtg cag tga aggacacggg gagaggctag ctccttgtcc tcctcagagc	1621
Asp Val Gln *	

agcaacctgg tattggactt cccttcttt catttgtacc aggtctcact caagaatctc 1681
 aatgaatatt tatgtggcaa ttatacaatt cccacaactg taaatacagg ctccatagaa 1741
 ttgctccccc tacactgtat ttacaaggc ttccggaaac cccactgaca cgccctttt 1801
 gcctcattaa atcaattgtt acttcaattt tgtcaactga gctaggacc gcctcgaaa 1861
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 tttttttttt tttttttttt cggagctggg gactgaaccc agggccttgc gcttgctagg 1981
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Leu Gly Gln Asn Leu Asp Leu Glu Ser Tyr Ser Pro Tyr Asn Asn Val	
35 40 45	
Gln Phe Pro Gln Val Gln Pro Gln Ile Ser Ser Ser Ser Tyr Tyr Ser	
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Asn Leu Gly Phe Tyr Pro Gln Gln Pro Glu Asp Trp Tyr Ser Pro Gly	
65 70 75 80	
Leu Tyr Glu Leu Arg Arg Met Pro Thr Glu Ser Val Tyr Gln Gly Glu	
85 90 95	
Thr Glu Val Ser Glu Met Pro Val Thr Lys Lys Pro Arg Met Ala Ala	
100 105 110	
Ser Ser Ala Gly Arg Ile Lys Gly Asp Glu Leu Cys Val Val Cys Gly	

115	120	125
Asp Arg Ala Ser Gly Tyr His	Tyr Asn Ala Leu Thr	Cys Glu Gly Cys
130	135	140
Lys Gly Phe Phe Arg Arg	Ser Ile Thr Lys Asn Ala Val Tyr Lys	Cys
145	150	155
Lys Asn Gly Gly Asn Cys Val Met Asp	Met Tyr Met Arg Arg	Lys Cys
165	170	175
Gln Asp Cys Arg Leu Arg Lys Cys	Arg Glu Met Gly Met	Leu Ala Glu
180	185	190
Cys Leu Leu Thr Glu Ile Gln Cys	Lys Ser Lys Arg	Leu Arg Lys Asn
195	200	205
Val Lys Gln His Ala Asp Gln Thr Val Asn Glu Asp	Ser Glu Gly Arg	
210	215	220
Asp Leu Arg Gln Val Thr Ser Thr Thr Lys	Leu Cys Arg Glu Lys	Thr
225	230	235
Glu Leu Thr Val Asp Gln Gln Thr Leu	Leu Asp Tyr Ile Met Asp Ser	
245	250	255
Tyr Ser Lys Gln Arg Met Pro Gln Glu	Ile Thr Asn Lys	Ile Leu Lys
260	265	270
Glu Glu Phe Ser Ala Glu Glu Asn Phe	Leu Ile Leu Thr	Glu Met Ala
275	280	285
Thr Ser His Val Gln Ile Leu Val Glu Phe Thr	Lys Arg Leu Pro Gly	
290	295	300
Phe Gln Thr Leu Asp His Glu Asp Gln Ile Ala	Leu Leu Lys Gly Ser	
305	310	315
Ala Val Glu Ala Met Phe Leu Arg Ser Ala Glu	Ile Phe Asn Lys	Lys
325	330	335
Leu Pro Ala Gly His Ala Asp Leu Leu	Glu Arg Ile Arg Lys Ser	
340	345	350
Gly Ile Ser Asp Glu Tyr Ile Thr Pro Met Phe Ser	Phe Tyr Lys Ser	
355	360	365
Val Gly Glu Leu Lys Met Thr Gln Glu Tyr Ala	Leu Leu Thr Ala	
370	375	380
Ile Val Ile Leu Ser Pro Asp Arg Gln Tyr	Ile Lys Asp Arg Glu Ala	
385	390	395
Val Glu Lys Leu Gln Glu Pro Leu Leu Asp Val	Leu Gln Lys Leu Cys	
405	410	415
Lys Ile Tyr Gln Pro Glu Asn Pro Gln His	Phe Ala Cys Leu Leu Gly	
420	425	430
Arg Leu Thr Glu Leu Arg Thr Phe Asn His His	Ala Glu Met Leu	
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Ile Trp Asp Val Gln		
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gtagaaggag taaaaagaaga aaagaagact tagaaacata gctcaaagtg aacactgctt 240
ctcttagttt cctggatttc ttctggacat ttccctcaaga tgaaaacttca gacactttgg 300
agttttttttaaagaccacc ataaagaaag tgcatttcaa ttgaaaaattt tgg atg 356

Met
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gga tca aaa atg aat ctc att gaa cat tcc cat tta cct acc aca gat		404
Gly Ser Lys Met Asn Leu Ile Glu His Ser His Leu Pro Thr Thr Asp		
5 10 15		
gaa ttt tct ttt tct gaa aat tta ttt ggt gtt tta aca gaa caa gtg		452
Glu Phe Ser Phe Ser Glu Asn Leu Phe Gly Val Leu Thr Glu Gln Val		
20 25 30		
gca ggt cct ctg gga cag aac ctg gaa gtg gaa cca tac tcg caa tac		500
Ala Gly Pro Leu Gly Gln Asn Leu Glu Val Glu Pro Tyr Ser Gln Tyr		
35 40 45		
agc aat gtt cag ttt ccc caa gtt caa cca cag att tcc tcg tca tcc		548
Ser Asn Val Gln Phe Pro Gln Val Gln Pro Gln Ile Ser Ser Ser Ser		
50 55 60 65		
tat tat tcc aac ctg ggt ttc tac ccc cag cag cct gaa gag tgg tac		596
Tyr Tyr Ser Asn Leu Gly Phe Tyr Pro Gln Gln Pro Glu Glu Trp Tyr		
70 75 80		
tct cct gga ata tat gaa ctc agg cgt atg cca gct gag act ctc tac		644
Ser Pro Gly Ile Tyr Glu Leu Arg Arg Met Pro Ala Glu Thr Leu Tyr		
85 90 95		
cag gga gaa act gag gta gca gag atg cct gta aca aag aag ccc cgc		692
Gln Gly Glu Thr Glu Val Ala Glu Met Pro Val Thr Lys Lys Pro Arg		
100 105 110		
atg ggc gcg tca gca ggg agg atc aaa ggg gat gag ctg tgt gtt gtt		740
Met Gly Ala Ser Ala Gly Arg Ile Lys Gly Asp Glu Leu Cys Val Val		
115 120 125		
tgt gga gac aga gcc tct gga tac cac tat aat gca ctg acc tgt gag		788
Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr Asn Ala Leu Thr Cys Glu		
130 135 140 145		
ggg tgt aaa ggt ttc ttc agg aga agc att acc aaa aac gct gtg tac		836
Gly Cys Lys Gly Phe Phe Arg Arg Ser Ile Thr Lys Asn Ala Val Tyr		
150 155 160		
aag tgt aaa aac ggg ggc aac tgt gtg atg gat atg tac atg cga aga		884
Lys Cys Lys Asn Gly Gly Asn Cys Val Met Asp Met Tyr Met Arg Arg		
165 170 175		
aag tgt caa gag tgt cga cta agg aaa tgc aaa gag atg gga atg ttg		932
Lys Cys Gln Glu Cys Arg Leu Arg Lys Cys Lys Glu Met Gly Met Leu		
180 185 190		
gct gaa tgc ttg tta act gaa att cag tgt aaa tct aag cga ctg aga		980
Ala Glu Cys Leu Leu Thr Glu Ile Gln Cys Lys Ser Lys Arg Leu Arg		
195 200 205		
aaa aat gtg aag cag cat gca gat cag acc gtg aat gaa gac agt gaa		1028
Lys Asn Val Lys Gln His Ala Asp Gln Thr Val Asn Glu Asp Ser Glu		
210 215 220 225		
ggt cgt gac ttg cga caa gtg acc tcg aca aca aag tca tgc agg gag		1076
Gly Arg Asp Leu Arg Gln Val Thr Ser Thr Thr Lys Ser Cys Arg Glu		
230 235 240		
aaa act gaa ctc acc cca gat caa cag act ctt cta cat ttt att atg		1124
Lys Thr Glu Leu Thr Pro Asp Gln Gln Thr Leu Leu His Phe Ile Met		
245 250 255		

gat tca tat aac aaa cag agg atg cct cag gaa ata aca aat aaa att		1172
Asp Ser Tyr Asn Lys Gln Arg Met Pro Gln Glu Ile Thr Asn Lys Ile		
260	265	270
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Leu Lys Glu Glu Phe Ser Ala Glu Glu Asn Phe Leu Ile Leu Thr Glu		
275	280	285
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Met Ala Thr Asn His Val Gln Val Leu Val Glu Phe Thr Lys Lys Leu		
290	295	300
305		
cca gga ttt cag act ttg gac cat gaa gac cag att gct ttg ctg aaa		1316
Pro Gly Phe Gln Thr Leu Asp His Glu Asp Gln Ile Ala Leu Leu Lys		
310	315	320
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Gly Ser Ala Val Glu Ala Met Phe Leu Arg Ser Ala Glu Ile Phe Asn		
325	330	335
aag aaa ctt ccg tct ggg cat tct gac cta ttg gaa gaa aga att cga		1412
Lys Lys Leu Pro Ser Gly His Ser Asp Leu Leu Glu Glu Arg Ile Arg		
340	345	350
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Asn Ser Gly Ile Ser Asp Glu Tyr Ile Thr Pro Met Phe Ser Phe Tyr		
355	360	365
aaa agt att ggg gaa ctg aaa atg act caa gag gag tat gct ctg ctt		1508
Lys Ser Ile Gly Glu Leu Lys Met Thr Gln Glu Tyr Ala Leu Leu		
370	375	380
385		
aca gca att gtt atc ctg tct cca gat aga caa tac ata aag gat aga		1556
Thr Ala Ile Val Ile Leu Ser Pro Asp Arg Gln Tyr Ile Lys Asp Arg		
390	395	400
gag gca gta gag aag ctt cag gag cca ctt ctt gat gtg cta caa aag		1604
Glu Ala Val Glu Lys Leu Gln Glu Pro Leu Leu Asp Val Leu Gln Lys		
405	410	415
ttg tgt aag att cac cag cct gaa aat cct caa cac ttt gcc tgt ctc		1652
Leu Cys Lys Ile His Gln Pro Glu Asn Pro Gln His Phe Ala Cys Leu		
420	425	430
ctg ggt cgc ctg act gaa tta cg aca ttc aat cat cac cac gct gag		1700
Leu Gly Arg Leu Thr Glu Leu Arg Thr Phe Asn His His His Ala Glu		
435	440	445
atg ctg atg tca tgg aga gta aac gac cac aag ttt acc cca ctt ctc		1748
Met Leu Met Ser Trp Arg Val Asn Asp His Lys Phe Thr Pro Leu Leu		
450	455	460
465		
tgt gaa atc tgg gac gtg cag tga tgggattac agggagggg tctagctcct		1802
Cys Glu Ile Trp Asp Val Gln *		
470		
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ctgttgaact agggaaaatc tcattttgct catcttacca tattgcatat attttattaa	2102	
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35 40 45
Tyr Ser Asn Val Gln Phe Pro Gln Val Gln Pro Gln Ile Ser Ser Ser
50 55 60
Ser Tyr Tyr Ser Asn Leu Gly Phe Tyr Pro Gln Gln Pro Glu Glu Trp
65 70 75 80
Tyr Ser Pro Gly Ile Tyr Glu Leu Arg Arg Met Pro Ala Glu Thr Leu
85 90 95
Tyr Gln Gly Glu Thr Glu Val Ala Glu Met Pro Val Thr Lys Lys Pro
100 105 110
Arg Met Gly Ala Ser Ala Gly Arg Ile Lys Gly Asp Glu Leu Cys Val
115 120 125
Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr Asn Ala Leu Thr Cys
130 135 140
Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Ile Thr Lys Asn Ala Val
145 150 155 160
Tyr Lys Cys Lys Asn Gly Gly Asn Cys Val Met Asp Met Tyr Met Arg
165 170 175
Arg Lys Cys Gln Glu Cys Arg Leu Arg Lys Cys Lys Glu Met Gly Met
180 185 190
Leu Ala Glu Cys Leu Leu Thr Glu Ile Gln Cys Lys Ser Lys Arg Leu
195 200 205
Arg Lys Asn Val Lys Gln His Ala Asp Gln Thr Val Asn Glu Asp Ser
210 215 220
Glu Gly Arg Asp Leu Arg Gln Val Thr Ser Thr Thr Lys Ser Cys Arg
225 230 235 240
Glu Lys Thr Glu Leu Thr Pro Asp Gln Gln Thr Leu Leu His Phe Ile
245 250 255
Met Asp Ser Tyr Asn Lys Gln Arg Met Pro Gln Glu Ile Thr Asn Lys
260 265 270
Ile Leu Lys Glu Glu Phe Ser Ala Glu Glu Asn Phe Leu Ile Leu Thr
275 280 285
Glu Met Ala Thr Asn His Val Gln Val Leu Val Glu Phe Thr Lys Lys
290 295 300
Leu Pro Gly Phe Gln Thr Leu Asp His Glu Asp Gln Ile Ala Leu Leu
305 310 315 320
Lys Gly Ser Ala Val Glu Ala Met Phe Leu Arg Ser Ala Glu Ile Phe
325 330 335
Asn Lys Lys Leu Pro Ser Gly His Ser Asp Leu Leu Glu Glu Arg Ile
340 345 350
Arg Asn Ser Gly Ile Ser Asp Glu Tyr Ile Thr Pro Met Phe Ser Phe
355 360 365
Tyr Lys Ser Ile Gly Glu Leu Lys Met Thr Gln Glu Glu Tyr Ala Leu
370 375 380
Leu Thr Ala Ile Val Ile Leu Ser Pro Asp Arg Gln Tyr Ile Lys Asp
385 390 395 400
Arg Glu Ala Val Glu Lys Leu Gln Glu Pro Leu Leu Asp Val Leu Gln
405 410 415
Lys Leu Cys Lys Ile His Gln Pro Glu Asn Pro Gln His Phe Ala Cys
420 425 430
Leu Leu Gly Arg Leu Thr Glu Leu Arg Thr Phe Asn His His His Ala
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gtg aac tcc tcc ctc acc tcc ccg acg ggg cga ggc tcc atg gct gcc 158 Val Asn Ser Ser Leu Thr Ser Pro Thr Gly Arg Gly Ser Met Ala Ala 15 20 25 30	158
ccc tcg ctg cac ccg tcc ctg ggg cct ggc atc ggc tcc ccg gga cag 206 Pro Ser Leu His Pro Ser Leu Gly Pro Gly Ile Gly Ser Pro Gly Gln 35 40 45	206
ctg cat tct ccc atc agc acc ctg agc tcc ccc atc aac ggc atg ggc 254 Leu His Ser Pro Ile Ser Thr Leu Ser Ser Pro Ile Asn Gly Met Gly 50 55 60	254
ccg cct ttc tcg gtc atc agc tcc ccc atg ggc ccc cac tcc atg tcg 302 Pro Pro Phe Ser Val Ile Ser Ser Pro Met Gly Pro His Ser Met Ser 65 70 75	302
gtg ccc acc aca ccc acc ctg ggc ttc agc act ggc agc ccc cag ctc 350 Val Pro Thr Thr Pro Thr Leu Gly Phe Ser Thr Gly Ser Pro Gln Leu 80 85 90	350
agc tca cct atg aac ccc gtc agc agc agc gag gac atc aag ccc ccc 398 Ser Ser Pro Met Asn Pro Val Ser Ser Glu Asp Ile Lys Pro Pro 95 100 105 110	398
ctg ggc ctc aat ggc gtc ctc aag gtc ccc gcc cac ccc tca gga aac 446 Leu Gly Leu Asn Gly Val Leu Lys Val Pro Ala His Pro Ser Gly Asn 115 120 125	446
atg gct tcc ttc acc aag cac atc tgc gcc atc tgc ggg gac cgc tcc 494 Met Ala Ser Phe Thr Lys His Ile Cys Ala Ile Cys Gly Asp Arg Ser 130 135 140	494
tca ggc aag cac tat gga gtg tac agc tgc gag ggg tgc aag ggc ttc 542 Ser Gly Lys His Tyr Gly Val Tyr Ser Cys Glu Gly Cys Lys Gly Phe 145 150 155	542
ttc aag cgg acg gtg cgc aag gac ctg acc tac acc tgc cgc gac aac 590 Phe Lys Arg Thr Val Arg Lys Asp Leu Thr Tyr Thr Cys Arg Asp Asn 160 165 170	590
aag gac tgc ctg att gac aag cgg cag cgg aac cgg tgc cag tac tgc 638 Lys Asp Cys Leu Ile Asp Lys Arg Gln Arg Asn Arg Cys Gln Tyr Cys 175 180 185 190	638
cgc tac cag aag tgc ctg gcc atg ggc atg aag cgg gaa gcc gtg cag 686 Arg Tyr Gln Lys Cys Leu Ala Met Gly Met Lys Arg Glu Ala Val Gln 195 200 205	686
gag gag cgg cag cgt ggc aag gac cgg aac gag aat gag gtg gag tgc 734 Glu Glu Arg Gln Arg Gly Lys Asp Arg Asn Glu Asn Glu Val Glu Ser	734

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ggg ctg aac ccc agc tcg ccg aac gac cct gtc acc aac att tgc caa Gly Leu Asn Pro Ser Ser Pro Asn Asp Pro Val Thr Asn Ile Cys Gln 255 260 265 270			878
gca gcc gac aaa cag ctt ttc acc ctg gtg gag tgg gcc aag cggt atc Ala Ala Asp Lys Gln Leu Phe Thr Leu Val Glu Trp Ala Lys Arg Ile 275 280 285			926
cca cac ttc tca gag ctg ccc ctg gac gac cag gtc atc ctg ctg cggt Pro His Phe Ser Glu Leu Pro Leu Asp Asp Gln Val Ile Leu Leu Arg 290 295 300			974
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gcc gtg aag gac ggg atc ctc ctg gcc acc ggg ctg cac gtc cac cggt Ala Val Lys Asp Gly Ile Leu Ala Thr Gly Leu His Val His Arg 320 325 330			1070
aac agc gcc cac agc gca ggg gtg ggc gcc atc ttt gac agg gtg ctg Asn Ser Ala His Ser Ala Gly Val Gly Ala Ile Phe Asp Arg Val Leu 335 340 345 350			1118
acg gag ctt gtg tcc aag atg cgg gac atg cag atg gac aag acg gag Thr Glu Leu Val Ser Lys Met Arg Asp Met Gln Met Asp Lys Thr Glu 355 360 365			1166
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tggtgcctt	tgcag	gccc	ccgt	aaagac	ccac	3607
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aacttgc	tttccc	tgg	tgc	tttgc	ccct	3727
cgcaccc	tggaa	acct	gtc	gtc	ccacc	3787
actgttccc	ggcactt	ggac	gttgc	tat	gttgc	3847
cagtgcgt	gtttgaaaa	gg	gtgt	gttgc	gttgc	3907
gtagaattt	tatttacca	gac	gtgt	gttgc	gttgc	3967
tttttgc	tatttatt	tttgg	tttgc	tttgc	tttgc	4027
catcagctca	ttagcc	gtgc	gttgc	ccgg	tttgc	4087
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ccgtggggc	cccagg	cc	gttgc	ccgg	ccgg	4507
ccctgtcg	gagct	gt	gttgc	ccgg	ccgg	4567
catgtatgt	ctgt	agac	gttgc	ccgg	ccgg	4627
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tgttgc	ctgt	gt	gttgc	ccgg	ccgg	5287
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Ser Pro Ile Ser Thr Leu Ser Ser Pro Ile Asn Gly Met Gly Pro Pro
50 55 60
Phe Ser Val Ile Ser Ser Pro Met Gly Pro His Ser Met Ser Val Pro
65 70 75 80
Thr Thr Pro Thr Leu Gly Phe Ser Thr Gly Ser Pro Gln Leu Ser Ser
85 90 95
Pro Met Asn Pro Val Ser Ser Ser Glu Asp Ile Lys Pro Pro Leu Gly
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Leu Asn Gly Val Leu Lys Val Pro Ala His Pro Ser Gly Asn Met Ala
115 120 125
Ser Phe Thr Lys His Ile Cys Ala Ile Cys Gly Asp Arg Ser Ser Gly
130 135 140
Lys His Tyr Gly Val Tyr Ser Cys Glu Gly Cys Lys Gly Phe Phe Lys
145 150 155 160
Arg Thr Val Arg Lys Asp Leu Thr Tyr Thr Cys Arg Asp Asn Lys Asp
165 170 175
Cys Leu Ile Asp Lys Arg Gln Arg Asn Arg Cys Gln Tyr Cys Arg Tyr
180 185 190
Gln Lys Cys Leu Ala Met Gly Met Lys Arg Glu Ala Val Gln Glu Glu
195 200 205
Arg Gln Arg Gly Lys Asp Arg Asn Glu Asn Glu Val Glu Ser Thr Ser
210 215 220
Ser Ala Asn Glu Asp Met Pro Val Glu Arg Ile Leu Glu Ala Glu Leu
225 230 235 240
Ala Val Glu Pro Lys Thr Glu Thr Tyr Val Glu Ala Asn Met Gly Leu
245 250 255
Asn Pro Ser Ser Pro Asn Asp Pro Val Thr Asn Ile Cys Gln Ala Ala
260 265 270
Asp Lys Gln Leu Phe Thr Leu Val Glu Trp Ala Lys Arg Ile Pro His
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Phe Ser Glu Leu Pro Leu Asp Asp Gln Val Ile Leu Leu Arg Ala Gly
290 295 300
Trp Asn Glu Leu Leu Ile Ala Ser Phe Ser His Arg Ser Ile Ala Val
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325 330 335
Ala His Ser Ala Gly Val Gly Ala Ile Phe Asp Arg Val Leu Thr Glu
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Leu Val Ser Lys Met Arg Asp Met Gln Met Asp Lys Thr Glu Leu Gly
355 360 365
Cys Leu Arg Ala Ile Val Leu Phe Asn Pro Asp Ser Lys Gly Leu Ser
370 375 380
Asn Pro Ala Glu Val Glu Ala Leu Arg Glu Lys Val Tyr Ala Ser Leu
385 390 395 400
Glu Ala Tyr Cys Lys His Lys Tyr Pro Glu Gln Pro Gly Arg Phe Ala
405 410 415
Lys Leu Leu Leu Arg Leu Pro Ala Leu Arg Ser Ile Gly Leu Lys Cys
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 atcacagctt agcgctctgt ggcctgcctg gcccacatcca tccaaatgt gtg gac 175
 Met Val Asp
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 aca gag agc ccc atc tgt cct ctc tcc cca ctg gag gca gat gac ctg 223
 Thr Glu Ser Pro Ile Cys Pro Leu Ser Pro Leu Glu Ala Asp Asp Leu
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 Glu Ser Pro Leu Ser Glu Glu Phe Leu Gln Glu Met Gly Asn Ile Gln
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 Glu Ile Ser Gln Ser Ile Gly Glu Glu Ser Ser Gly Ser Phe Gly Phe
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 Ala Asp Tyr Gln Tyr Leu Gly Ser Cys Pro Gly Ser Glu Gly Ser Val
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 atc aca gac acc ctc tct cca cgt tcc agc cct tcc tca gtc agc tgc 415
 Ile Thr Asp Thr Leu Ser Pro Arg Ser Ser Pro Ser Ser Val Ser Cys
 70 75 80
 ccc gtg atc ccc gcc agc acg gac gag tcc ccc ggc agt gcc ctg aac 463
 Pro Val Ile Pro Ala Ser Thr Asp Glu Ser Pro Gly Ser Ala Leu Asn
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 atc gag tgt cga ata tgt ggg gac aag gcc tca ggg tac cac tac gga 511
 Ile Glu Cys Arg Ile Cys Gly Asp Lys Ala Ser Gly Tyr His Tyr Gly
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 gtt cac gca tgt gaa ggc tgt aag ggc ttc ttt cgg cga act att cgg 559
 Val His Ala Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Thr Ile Arg
 120 125 130
 ctg aag ctg gtg tac gac aag tgt gat cgg agc tgc aag att cag aag 607
 Leu Lys Leu Val Tyr Asp Lys Cys Asp Arg Ser Cys Lys Ile Gln Lys
 135 140 145
 aag aac cgg aac aaa tgc cag tac tgc cgt ttt cac aag tgc ctg tct 655
 Lys Asn Arg Asn Lys Cys Gln Tyr Cys Arg Phe His Lys Cys Leu Ser
 150 155 160
 gtc ggg atg tca cac aat gca att cgc ttt gga aga atg cca aga tct 703
 Val Gly Met Ser His Asn Ala Ile Arg Phe Gly Arg Met Pro Arg Ser
 165 170 175
 gaa aaa gca aaa ctg aaa gca gaa att ctt acc tgt gaa cac gac ctg 751
 Glu Lys Ala Lys Leu Lys Ala Glu Ile Leu Thr Cys Glu His Asp Leu
 180 185 190 195
 aaa gat tcg gaa act gca gac ctc aaa tct ctg ggc aag aga atc cac 799

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Glu	Ala	Tyr	Leu	Lys	Asn	Phe	Asn	Met	Asn	Lys	Val	Lys	Ala	Arg	Val		
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ata	ctc	g	g	a	a	g	a	c	a	c	cc	c	t	t	g	895	
Ile	Leu	Ala	Gly	Lys	Thr	Ser	Asn	Asn	Pro	Pro	Phe	Val	Ile	His	Asp		
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Met	Glu	Thr	Leu	Cys	Met	Ala	Glu	Lys	Thr	Leu	Val	Ala	Lys	Met	Val		
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gcc	aac	ggc	gtc	gaa	gac	aaa	gag	gca	gag	gtc	cga	ttc	ttc	cac	tgc	991	
Ala	Asn	Gly	Val	Glu	Asp	Lys	Glu	Ala	Glu	Val	Arg	Phe	Phe	His	Cys		
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Cys	Gln	Cys	Met	Ser	Val	Glu	Thr	Val	Thr	Glu	Leu	Thr	Glu	Phe	Ala		
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aag	gct	atc	cca	ggc	ttt	gca	aac	ttg	gac	ttg	aac	gac	caa	gtc	'acc	1087	
Lys	Ala	Ile	Pro	Gly	Phe	Ala	Asn	Leu	Asp	Leu	Asn	Asp	Gln	Val	Thr		
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ttg	cta	aag	ta	c	gg	gt	ta	g	aa	g	cc	at	tc	tc	tc	1135	
Leu	Leu	Lys	Tyr	Gly	Val	Tyr	Glu	Ala	Ile	Phe	Thr	Met	Leu	Ser	Ser		
				310				315					320				
ttg	atg	aac	aaa	gac	ggg	atg	ctg	atc	g	cc	aat	gg	ttt	atc		1183	
Leu	Met	Asn	Lys	Asp	Gly	Met	Leu	Ile	Ala	Tyr	Gly	Asn	Gly	Phe	Ile		
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aca	cgc	gag	ttc	ctt	aag	aac	ctg	agg	aag	cc	ttc	tgt	gac	atc	atg	1231	
Thr	Arg	Glu	Phe	Leu	Lys	Asn	Leu	Arg	Lys	Pro	Phe	Cys	Asp	Ile	Met		
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gaa	ccc	aag	ttt	gac	ttc	gct	atg	aag	ttc	aat	gcc	tta	gaa	ctg	gat	1279	
Glu	Pro	Lys	Phe	Asp	Phe	Ala	Met	Lys	Phe	Asn	Ala	Leu	Glu	Leu	Asp		
				360				365					370				
gac	agt	gac	att	tcc	ctg	ttt	gtg	gct	gct	ata	att	tgc	tgt	gga	gat	1327	
Asp	Ser	Asp	Ile	Ser	Leu	Phe	Val	Ala	Ala	Ile	Ile	Cys	Cys	Gly	Asp		
				375				380					385				
cgg	cct	ggc	ctt	cta	aac	ata	g	gc	ta	tt	gag	aag	ttg	cag	gag	1375	
Arg	Pro	Gly	Leu	Leu	Asn	Ile	Gly	Tyr	Ile	Glu	Lys	Leu	Gln	Glu	Gly		
				390				395					400				
att	gtg	cac	gtg	ctt	aag	ctc	cac	ctg	cag	agc	aac	cat	cca	gat	gac	1423	
Ile	Val	His	Val	Leu	Lys	Leu	His	Leu	Gln	Ser	Asn	His	Pro	Asp	Asp		
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acc	ttc	ctc	ttc	cca	aag	ctc	ctt	caa	aaa	atg	gtg	gac	ctt	cg	cg	1471	
Thr	Phe	Leu	Phe	Pro	Lys	Leu	Leu	Gln	Lys	Met	Val	Asp	Leu	Arg	Gln		
				420				425					430			435	
ctg	gtc	acg	gag	cat	g	gc	c	tg	c	atc	aag	aag	acc	gag		1519	
Leu	Val	Thr	Glu	His	A	Ala	Gln	Leu	Val	Gln	Val	Ile	Lys	Lys	Thr	Glu	
				440				445					450				
tcc	gac	gca	g	ctg	cac	cc	ctg	ttg	caa	gag	atc	tac	aga	gac	atg	1567	
Ser	Asp	Ala	Ala	Leu	His	Pro	Leu	Leu	Gln	Glu	Ile	Tyr	Arg	Asp	Met		
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Tyr *

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<213> Mus musculus

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35 40 45
Phe Gly Phe Ala Asp Tyr Gln Tyr Leu Gly Ser Cys Pro Gly Ser Glu
50 55 60
Gly Ser Val Ile Thr Asp Thr Leu Ser Pro Arg Ser Ser Pro Ser Ser
65 70 75 80
Val Ser Cys Pro Val Ile Pro Ala Ser Thr Asp Glu Ser Pro Gly Ser
85 90 95
Ala Leu Asn Ile Glu Cys Arg Ile Cys Gly Asp Lys Ala Ser Gly Tyr
100 105 110
His Tyr Gly Val His Ala Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg
115 120 125
Thr Ile Arg Leu Lys Leu Val Tyr Asp Lys Cys Asp Arg Ser Cys Lys
130 135 140
Ile Gln Lys Lys Asn Arg Asn Lys Cys Gln Tyr Cys Arg Phe His Lys
145 150 155 160
Cys Leu Ser Val Gly Met Ser His Asn Ala Ile Arg Phe Gly Arg Met
165 170 175
Pro Arg Ser Glu Lys Ala Lys Leu Lys Ala Glu Ile Leu Thr Cys Glu
180 185 190
His Asp Leu Lys Asp Ser Glu Thr Ala Asp Leu Lys Ser Leu Gly Lys
195 200 205
Arg Ile His Glu Ala Tyr Leu Lys Asn Phe Asn Met Asn Lys Val Lys
210 215 220
Ala Arg Val Ile Leu Ala Gly Lys Thr Ser Asn Asn Pro Pro Phe Val
225 230 235 240
Ile His Asp Met Glu Thr Leu Cys Met Ala Glu Lys Thr Leu Val Ala
245 250 255
Lys Met Val Ala Asn Gly Val Glu Asp Lys Glu Ala Glu Val Arg Phe
260 265 270
Phe His Cys Cys Gln Cys Met Ser Val Glu Thr Val Thr Glu Leu Thr
275 280 285
Glu Phe Ala Lys Ala Ile Pro Gly Phe Ala Asn Leu Asp Leu Asn Asp
290 295 300
Gln Val Thr Leu Leu Lys Tyr Gly Val Tyr Glu Ala Ile Phe Thr Met
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Leu Ser Ser Leu Met Asn Lys Asp Gly Met Leu Ile Ala Tyr Gly Asn
325 330 335
Gly Phe Ile Thr Arg Glu Phe Leu Lys Asn Leu Arg Lys Pro Phe Cys
340 345 350
Asp Ile Met Glu Pro Lys Phe Asp Phe Ala Met Lys Phe Asn Ala Leu
355 360 365
Glu Leu Asp Asp Ser Asp Ile Ser Leu Phe Val Ala Ala Ile Ile Cys
370 375 380

Cys Gly Asp Arg Pro Gly Leu Leu Asn Ile Gly Tyr Ile Glu Lys Leu
 385 390 395 400
 Gln Glu Gly Ile Val His Val Leu Lys Leu His Leu Gln Ser Asn His
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 Pro Asp Asp Thr Phe Leu Phe Pro Lys Leu Leu Gln Lys Met Val Asp
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 Leu Arg Gln Leu Val Thr Glu His Ala Gln Leu Val Gln Val Ile Lys
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35	40	45

tcc	cct	tcc	tcc	ctg	ctg	gac	cag	ctg	cag	atg	ggc	tgt	gat	ggg	gcc	192
Ser	Pro	Ser	Ser	Leu	Leu	Asp	Gln	Leu	Gln	Met	Gly	Cys	Asp	Gly	Ala	
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tca	ggc	ggc	agc	ctc	aac	atg	gaa	tgt	cgg	gtg	tgc	ggg	gac	aag	gcc	240
Ser	Gly	Gly	Ser	Leu	Asn	Met	Glu	Cys	Arg	Val	Cys	Gly	Asp	Lys	Ala	
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ttc cgc cg^a aca atc cg^c atg aag ctc gag tat gag aag tgc gat cg^g 336
 Phe Arg Arg Thr Ile Arg Met Lys Leu Glu Tyr Glu Lys Cys Asp Arg
 100 105 110

atc tgc aag atc cag aag aag aac cgc aac aag tgt cag tac tgc cgc 384
Ile Cys Lys Ile Gln Lys Lys Asn Arg Asn Lys Cys Gln Tyr Cys Arg
115 120 125

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Phe Gln Lys Cys Leu Ala Leu Gly Met Ser His Asn Ala Ile Arg Phe
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Phe Ser Lys His Ile Tyr Asn Ala Tyr Leu Lys Asn Phe Asn Met Thr	
180 185 190	
aaa aag aag gcc cggtt cgg agc atc ctc acc ggc aag tcc agc cac aac gca	624
Lys Lys Ala Arg Ser Ile Leu Thr Gly Lys Ser Ser His Asn Ala	
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Pro Phe Val Ile His Asp Ile Glu Thr Leu Trp Gln Ala Glu Lys Gly	
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Leu Val Trp Lys Gln Leu Val Asn Gly Leu Pro Pro Tyr Asn Glu Ile	
225 230 235 240	
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Ser Val His Val Phe Tyr Arg Cys Gln Ser Thr Thr Val Glu Thr Val	
245 250 255	
cga gag ctc acc gag ttc gcc aag aac atc ccc aac ttc agc agc ctc	816
Arg Glu Leu Thr Glu Phe Ala Lys Asn Ile Pro Asn Phe Ser Ser Leu	
260 265 270	
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Phe Leu Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly Val His Glu Ala	
275 280 285	
atc ttt gcc atg ctg gcc tcc atc gtc aac aaa gac ggg ctg ctg gtg	912
Ile Phe Ala Met Leu Ala Ser Ile Val Asn Lys Asp Gly Leu Leu Val	
290 295 300	
gcc aac ggc agt ggc ttc gtc acc cac gag ttc ttg cga agt ctc cgc	960
Ala Asn Gly Ser Gly Phe Val Thr His Glu Phe Leu Arg Ser Leu Arg	
305 310 315 320	
aag ccc ttc agt gac atc att gag ccc aag ttc gag ttt gct gtc aag	1008
Lys Pro Phe Ser Asp Ile Ile Glu Pro Lys Phe Glu Phe Ala Val Lys	
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Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Leu Phe Ile Ala	
340 345 350	
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Ala Ile Ile Leu Cys Gly Asp Arg Pro Gly Leu Met Asn Val Pro Gln	
355 360 365	
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Val Glu Ala Ile Gln Asp Thr Ile Leu Arg Ala Leu Glu Phe His Leu	
370 375 380	
cag gtc aac cac cct gac agc cag tac ctc ttc ccc aag ctg ctg cag	1200
Gln Val Asn His Pro Asp Ser Gln Tyr Leu Phe Pro Lys Leu Leu Gln	
385 390 395 400	
aag atg gca gac ctg cgg cag ctg gtc act gag cat gcc cag atg atg	1248
Lys Met Ala Asp Leu Arg Gln Leu Val Thr Glu His Ala Gln Met Met	
405 410 415	
cag tgg cta aag aag acg gag agt gag acc ttg ctg cac ccc ctg ctc	1296
Gln Trp Leu Lys Lys Thr Glu Ser Glu Thr Leu Leu His Pro Leu Leu	

420

425

430

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1323

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 Ser Pro Ser Ser Leu Leu Asp Gln Leu Gln Met Gly Cys Asp Gly Ala
 50 55 60
 Ser Gly Gly Ser Leu Asn Met Glu Cys Arg Val Cys Gly Asp Lys Ala
 65 70 75 80
 Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys Gly Phe
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 Phe Arg Arg Thr Ile Arg Met Lys Leu Glu Tyr Glu Lys Cys Asp Arg
 100 105 110
 Ile Cys Lys Ile Gln Lys Lys Asn Arg Asn Lys Cys Gln Tyr Cys Arg
 115 120 125
 Phe Gln Lys Cys Leu Ala Leu Gly Met Ser His Asn Ala Ile Arg Phe
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 Gly Arg Met Pro Asp Gly Glu Lys Arg Lys Leu Val Ala Gly Leu Thr
 145 150 155 160
 Ala Ser Glu Gly Cys Gln His Asn Pro Gln Leu Ala Asp Leu Lys Ala
 165 170 175
 Phe Ser Lys His Ile Tyr Asn Ala Tyr Leu Lys Asn Phe Asn Met Thr
 180 185 190
 Lys Lys Lys Ala Arg Ser Ile Leu Thr Gly Lys Ser Ser His Asn Ala
 195 200 205
 Pro Phe Val Ile His Asp Ile Glu Thr Leu Trp Gln Ala Glu Lys Gly
 210 215 220
 Leu Val Trp Lys Gln Leu Val Asn Gly Leu Pro Pro Tyr Asn Glu Ile
 225 230 235 240
 Ser Val His Val Phe Tyr Arg Cys Gln Ser Thr Thr Val Glu Thr Val
 245 250 255
 Arg Glu Leu Thr Glu Phe Ala Lys Asn Ile Pro Asn Phe Ser Ser Leu
 260 265 270
 Phe Leu Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly Val His Glu Ala
 275 280 285
 Ile Phe Ala Met Leu Ala Ser Ile Val Asn Lys Asp Gly Leu Leu Val
 290 295 300
 Ala Asn Gly Ser Gly Phe Val Thr His Glu Phe Leu Arg Ser Leu Arg
 305 310 315 320
 Lys Pro Phe Ser Asp Ile Ile Glu Pro Lys Phe Glu Phe Ala Val Lys
 325 330 335
 Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Leu Phe Ile Ala
 340 345 350
 Ala Ile Ile Leu Cys Gly Asp Arg Pro Gly Leu Met Asn Val Pro Gln
 355 360 365
 Val Glu Ala Ile Gln Asp Thr Ile Leu Arg Ala Leu Glu Phe His Leu
 370 375 380
 Gln Val Asn His Pro Asp Ser Gln Tyr Leu Phe Pro Lys Leu Leu Gln
 385 390 395 400
 Lys Met Ala Asp Leu Arg Gln Leu Val Thr Glu His Ala Gln Met Met
 405 410 415
 Gln Trp Leu Lys Lys Thr Glu Ser Glu Thr Leu Leu His Pro Leu Leu
 420 425 430

Gln Glu Ile Tyr Lys Asp Met Tyr
435 440

<210> 15
<211> 1827
<212> DNA
<213> Homo Sapien

<220>
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<222> (292) ... (1683)

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<309> 2002-05-08

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attcctgact aatcccagag ggctggcca gcctgtgctc cccgggctgc taggaagcga 180
tgaccactt tggtagccca agttgaagaa agccgggctg tgccctggag ccgagagagg 240
cggtaatatt tagaagctgc acaggagagg aacatgaact gacgagtaaa c atg tat 297
Met Tyr
1
gga aat tat tct cac ttc atg aag ttt ccc gca ggc tat gga ggc tcc 345
Gly Asn Tyr Ser His Phe Met Lys Phe Pro Ala Gly Tyr Gly Gly Ser
5 10 15
cct ggc cac act ggc tct aca tcc atg agc cca tca gca gcc ttg tcc 393
Pro Gly His Thr Gly Ser Thr Ser Met Ser Pro Ser Ala Ala Leu Ser
20 25 30
aca ggg aag cca atg gac agc cac ccc agc tac aca gat acc cca gtg 441
Thr Gly Lys Pro Met Asp Ser His Pro Ser Tyr Thr Asp Thr Pro Val
35 40 45 50
agt gcc cca cgg act ctg agt gca gtg ggg acc ccc ctc aat gcc ctg 489
Ser Ala Pro Arg Thr Leu Ser Ala Val Gly Thr Pro Leu Asn Ala Leu
55 60 65
ggc tct cca tat cga gtc atc acc tct gcc atg ggc cca ccc tca gga 537
Gly Ser Pro Tyr Arg Val Ile Thr Ser Ala Met Gly Pro Pro Ser Gly
70 75 80
gca ctt gca gcg cct cca gga atc aac ttg gtt gcc cca ccc agc tct 585
Ala Leu Ala Ala Pro Pro Gly Ile Asn Leu Val Ala Pro Pro Ser Ser
85 90 95
cag cta aat gtg gtc aac agt gtc agc agt tca gag gac atc aag ccc 633
Gln Leu Asn Val Val Asn Ser Val Ser Ser Glu Asp Ile Lys Pro
100 105 110
tta cca ggg ctt ccc ggg att gga aac atg aac tac cca tcc acc agc 681
Leu Pro Gly Leu Pro Gly Ile Gly Asn Met Asn Tyr Pro Ser Thr Ser
115 120 125 130
ccc gga tct ctg gtt aaa cac atc tgt gcc atc tgt gga gac aga tcc 729
Pro Gly Ser Leu Val Lys His Ile Cys Ala Ile Cys Gly Asp Arg Ser
135 140 145
tca gga aag cac tac ggg gta tac agt tgt gaa ggc tgc aaa ggg ttc 777
Ser Gly Lys His Tyr Gly Val Tyr Ser Cys Glu Gly Cys Lys Gly Phe
150 155 160
ttc aag agg acg ata agg aag gac ctc atc tac acg tgt cgg gat aat 825

Phe Lys Arg Thr Ile Arg Lys Asp Leu Ile Tyr Thr Cys Arg Asp Asn			
165	170	175	
aaa gac tgc ctc att gac aag cgt cag cgc aac cgc tgc cag tac tgt	Lys Asp Cys Leu Ile Asp Lys Arg Gln Arg Asn Arg Cys Gln Tyr Cys	873	
180	185	190	
cgc tat cag aag tgc ctt gtc atg ggc atg aag agg gaa gct gtg caa	Arg Tyr Gln Lys Cys Leu Val Met Gly Met Lys Arg Glu Ala Val Gln	921	
195	200	205	210
gaa gaa aga cag agg agc cga gag cga gct gag agt gag gca gaa tgt	Glu Glu Arg Gln Arg Ser Arg Glu Arg Ala Glu Ser Glu Ala Glu Cys	969	
215	220	225	
gct acc agt ggt cat gaa gac atg cct gtg gag agg att cta gaa gct	Ala Thr Ser Gly His Glu Asp Met Pro Val Glu Arg Ile Leu Glu Ala	1017	
230	235	240	
gaa ctt gct gtt gaa cca aag aca gaa tcc tat ggt gac atg aat atg	Glu Leu Ala Val Glu Pro Lys Thr Glu Ser Tyr Gly Asp Met Asn Met	1065	
245	250	255	
gag aac tcg aca aat gac cct gtt acc aac ata tgt cat gct gct gac	Glu Asn Ser Thr Asn Asp Pro Val Thr Asn Ile Cys His Ala Ala Asp	1113	
260	265	270	
aag cag ctt ttc acc ctc gtt gaa tgg gcc aag cgt att ccc cac ttc	Lys Gln Leu Phe Thr Leu Val Glu Trp Ala Lys Arg Ile Pro His Phe	1161	
275	280	285	290
tct gac ctc acc ttg gag gac cag gtc att ttg ctt cg gca ggg tgg	Ser Asp Leu Thr Leu Glu Asp Gln Val Ile Leu Leu Arg Ala Gly Trp	1209	
295	300	305	
aat gaa ttg ctg att gcc tct ttc tcc cac cgc tca gtt tcc gtg cag	Asn Glu Leu Leu Ile Ala Ser Phe Ser His Arg Ser Val Ser Val Gln	1257	
310	315	320	
gat ggc atc ctt ctg gcc acg ggt tta cat gtc cac cgg agc agt gcc	Asp Gly Ile Leu Leu Ala Thr Gly Leu His Val His Arg Ser Ser Ala	1305	
325	330	335	
cac agt gct ggg gtc ggc tcc atc ttt gac aga gtc cta act gag ctg	His Ser Ala Gly Val Gly Ser Ile Phe Asp Arg Val Leu Thr Glu Leu	1353	
340	345	350	
gtt tcc aaa atg aaa gac atg cag atg gac aag tcg gaa ctg gga tgc	Val Ser Lys Met Lys Asp Met Gln Met Asp Lys Ser Glu Leu Gly Cys	1401	
355	360	365	370
ctg cga gcc att gta ctc ttt aac cca gat gcc aag ggc ctg tcc aac	Leu Arg Ala Ile Val Leu Phe Asn Pro Asp Ala Lys Gly Leu Ser Asn	1449	
375	380	385	
ccc tct gag gtg gag act ctg cga gag aag gtt tat gcc acc ctt gag	Pro Ser Glu Val Glu Thr Leu Arg Glu Lys Val Tyr Ala Thr Leu Glu	1497	
390	395	400	
gcc tac acc aag cag aag tat ccg gaa cag cca ggc agg ttt gcc aag	Ala Tyr Thr Lys Gln Lys Tyr Pro Glu Gln Pro Gly Arg Phe Ala Lys	1545	
405	410	415	
ctg ctg cgc ctc cca gct ctg cgt tcc att ggc ttg aaa tgc ctg	Leu Leu Leu Arg Leu Pro Ala Leu Arg Ser Ile Gly Leu Lys Cys Leu	1593	
420	425	430	

gag cac ctc ttc ttc aag ctc atc ggg gac acc ccc att gac acc 1641
 Glu His Leu Phe Phe Phe Lys Leu Ile Gly Asp Thr Pro Ile Asp Thr
 435 440 445 450
 ttc ctc atg gag atg ttg gag acc ccg ctg cag atc acc tga 1683
 Phe Leu Met Glu Met Leu Glu Thr Pro Leu Gln Ile Thr *
 455 460

gccccaccag ccacagcctc cccacccagg atgacccctg ggcaggtgtg tgtggacccc 1743
 caccctgcac tttccctcac ctcacccctt gaccccttc ctgtcccaa aatgtgatgc 1803
 ttataataaa gaaaacctt ctac 1827

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 <211> 463
 <212> PRT
 <213> Homo Sapien

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 20 25 30
 Leu Ser Thr Gly Lys Pro Met Asp Ser His Pro Ser Tyr Thr Asp Thr
 35 40 45
 Pro Val Ser Ala Pro Arg Thr Leu Ser Ala Val Gly Thr Pro Leu Asn
 50 55 60
 Ala Leu Gly Ser Pro Tyr Arg Val Ile Thr Ser Ala Met Gly Pro Pro
 65 70 75 80
 Ser Gly Ala Leu Ala Ala Pro Pro Gly Ile Asn Leu Val Ala Pro Pro
 85 90 95
 Ser Ser Gln Leu Asn Val Val Asn Ser Val Ser Ser Glu Asp Ile
 100 105 110
 Lys Pro Leu Pro Gly Leu Pro Gly Ile Gly Asn Met Asn Tyr Pro Ser
 115 120 125
 Thr Ser Pro Gly Ser Leu Val Lys His Ile Cys Ala Ile Cys Gly Asp
 130 135 140
 Arg Ser Ser Gly Lys His Tyr Gly Val Tyr Ser Cys Glu Gly Cys Lys
 145 150 155 160
 Gly Phe Phe Lys Arg Thr Ile Arg Lys Asp Leu Ile Tyr Thr Cys Arg
 165 170 175
 Asp Asn Lys Asp Cys Leu Ile Asp Lys Arg Gln Arg Asn Arg Cys Gln
 180 185 190
 Tyr Cys Arg Tyr Gln Lys Cys Leu Val Met Gly Met Lys Arg Glu Ala
 195 200 205
 Val Gln Glu Glu Arg Gln Arg Ser Arg Glu Arg Ala Glu Ser Glu Ala
 210 215 220
 Glu Cys Ala Thr Ser Gly His Glu Asp Met Pro Val Glu Arg Ile Leu
 225 230 235 240
 Glu Ala Glu Leu Ala Val Glu Pro Lys Thr Glu Ser Tyr Gly Asp Met
 245 250 255
 Asn Met Glu Asn Ser Thr Asn Asp Pro Val Thr Asn Ile Cys His Ala
 260 265 270
 Ala Asp Lys Gln Leu Phe Thr Leu Val Glu Trp Ala Lys Arg Ile Pro
 275 280 285
 His Phe Ser Asp Leu Thr Leu Glu Asp Gln Val Ile Leu Leu Arg Ala
 290 295 300
 Gly Trp Asn Glu Leu Leu Ile Ala Ser Phe Ser His Arg Ser Val Ser
 305 310 315 320
 Val Gln Asp Gly Ile Leu Leu Ala Thr Gly Leu His Val His Arg Ser
 325 330 335
 Ser Ala His Ser Ala Gly Val Gly Ser Ile Phe Asp Arg Val Leu Thr
 340 345 350
 Glu Leu Val Ser Lys Met Lys Asp Met Gln Met Asp Lys Ser Glu Leu
 355 360 365
 Gly Cys Leu Arg Ala Ile Val Leu Phe Asn Pro Asp Ala Lys Gly Leu
 370 375 380
 Ser Asn Pro Ser Glu Val Glu Thr Leu Arg Glu Lys Val Tyr Ala Thr

385	390	395	400
Leu Glu Ala Tyr Thr Lys Gln Lys Tyr Pro Glu Gln Pro Gly Arg Phe			
405	410	415	
Ala Lys Leu Leu Leu Arg Leu Pro Ala Leu Arg Ser Ile Gly Leu Lys			
420	425	430	
Cys Leu Glu His Leu Phe Phe Phe Lys Leu Ile Gly Asp Thr Pro Ile			
435	440	445	
Asp Thr Phe Leu Met Glu Met Leu Glu Thr Pro Leu Gln Ile Thr			
450	455	460	

<210> 17
<211> 1330
<212> DNA
<213> Homo Sapien

<220>
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<222> (97) . . . (837)

<300>
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<309> 2002-02-06

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gaatgtgcat tgcagggcct tgcttagtgg taggga atg att tcc atc act tct	114		
Met Ile Ser Ile Thr Ser			
1		5	
gtg aca ttc tgc ttc cca ata agt ctt cct gtg act tcc cta ttt ccc	162		
Val Thr Phe Cys Phe Pro Ile Ser Leu Pro Val Thr Ser Leu Phe Pro			
10	15	20	
cca tcc cag att aac tca aca gtg tca ctc cct ggg ggt ggg tct ggc	210		
Pro Ser Gln Ile Asn Ser Thr Val Ser Leu Pro Gly Gly Ser Gly			
25	30	35	
ccc cct gaa gat gtg aag cca cca gtc tta ggg gtc cgg ggc ctg cac	258		
Pro Pro Glu Asp Val Lys Pro Pro Val Leu Gly Val Arg Gly Leu His			
40	45	50	
tgt cca ccc cct cca ggt ggc cct ggg gct ggc aaa cgg cta tgt gca	306		
Cys Pro Pro Pro Gly Gly Pro Gly Ala Gly Lys Arg Leu Cys Ala			
55	60	65	70
atc tgc ggg gac aga agc tca ggc aaa cac tac ggg gtt tac agc tgt	354		
Ile Cys Gly Asp Arg Ser Ser Gly Lys His Tyr Gly Val Tyr Ser Cys			
75	80	85	
gag ggt tgc aag ggc ttc ttc aaa cgc acc atc cgc aaa gac ctt aca	402		
Glu Gly Cys Lys Gly Phe Phe Lys Arg Thr Ile Arg Lys Asp Leu Thr			
90	95	100	
tac tct tgc cgg gac aac aaa gac tgc aca gtg gac aag cgc cag cgg	450		
Tyr Ser Cys Arg Asp Asn Lys Asp Cys Thr Val Asp Lys Arg Gln Arg			
105	110	115	
aac cgc tgt cag tac tgc cgc tat cag aag tgc ctg gcc act ggc atg	498		
Asn Arg Cys Gln Tyr Cys Arg Tyr Gln Lys Cys Leu Ala Thr Gly Met			
120	125	130	
aag agg gag gcg gta cag gag gag cgt cag cgg gga aag gac aag gat	546		
Lys Arg Glu Ala Val Gln Glu Glu Arg Gln Arg Gly Lys Asp Lys Asp			
135	140	145	150
ggg gat ggg gag ggg gct ggg gga gcc ccc gag gag atg cct gtg gac	594		

Gly Asp Gly Glu Gly Ala Gly Gly Ala Pro Glu Glu Met Pro Val Asp			
155	160	165	
agg atc ctg gag gca gag ctt gct gtg gaa cag aag agt gac cag ggc		642	
Arg Ile Leu Glu Ala Glu Leu Ala Val Glu Gln Lys Ser Asp Gln Gly			
170	175	180	
gtt gag ggt cct ggg gga acc ggg ggt agc ggc agc agc gtg agt gtt		690	
Val Glu Gly Pro Gly Gly Thr Gly Ser Gly Ser Ser Val Ser Val			
185	190	195	
ggg gtc aat cca ctc tcc ttc gtg atg ggg gtt ggg gga ggc agt cta		738	
Gly Val Asn Pro Leu Ser Phe Val Met Gly Val Gly Gly Ser Leu			
200	205	210	
ggt ctg ttc tac atc ccc tcc ccc tcc ttt ccc ctc ata acc ttc cta		786	
Gly Leu Phe Tyr Ile Pro Ser Pro Ser Phe Pro Leu Ile Thr Phe Leu			
215	220	225	230
aca cta ctt ggg act gga ggt gct gcc aaa caa ggt ctt tca aac atc		834	
Thr Leu Leu Gly Thr Gly Gly Ala Ala Lys Gln Gly Leu Ser Asn Ile			
235	240	245	
tga ggtggatgtg atagctcctt ctgtctccac tccccaaaca acccaactggc		887	
*			

agaaccatag gcatgtccca aataaataat tgtttgact aatgccagaa gagaagactc 947
 acttacaggg attgggttgg atggggctca caggaagact atatgttaagg aggggggtgtc 1007
 aaaaggctct tacaaggggg ctcccagcat atctcaaaaat cttccataac tcttacccccc 1067
 gtccccctgca gccaaatgac cctgtgacta acatctgtca ggcagctgac aaacagctat 1127
 tcacgcttgt tgagtggcg aagaggatcc cacactttc ctccttgctt ctggatgatc 1187
 aggtcatatt gctgcgggca ggtcagtgac cttggatccc tttgacttct tgacatttga 1247
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 gccaaacttg ctgacccctgc cac 1330

<210> 18
 <211> 246
 <212> PRT
 <213> Homo Sapien

<400> 18
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 1 5 10 15
 Val Thr Ser Leu Phe Pro Pro Ser Gln Ile Asn Ser Thr Val Ser Leu
 20 25 30
 Pro Gly Gly Ser Gly Pro Pro Glu Asp Val Lys Pro Pro Val Leu
 35 40 45
 Gly Val Arg Gly Leu His Cys Pro Pro Pro Gly Gly Pro Gly Ala
 50 55 60
 Gly Lys Arg Leu Cys Ala Ile Cys Gly Asp Arg Ser Ser Gly Lys His
 65 70 75 80
 Tyr Gly Val Tyr Ser Cys Glu Gly Cys Lys Gly Phe Phe Lys Arg Thr
 85 90 95
 Ile Arg Lys Asp Leu Thr Tyr Ser Cys Arg Asp Asn Lys Asp Cys Thr
 100 105 110
 Val Asp Lys Arg Gln Arg Asn Arg Cys Gln Tyr Cys Arg Tyr Gln Lys
 115 120 125
 Cys Leu Ala Thr Gly Met Lys Arg Glu Ala Val Gln Glu Glu Arg Gln
 130 135 140
 Arg Gly Lys Asp Lys Asp Gly Asp Gly Glu Gly Ala Gly Gly Ala Pro
 145 150 155 160
 Glu Glu Met Pro Val Asp Arg Ile Leu Glu Ala Glu Leu Ala Val Glu
 165 170 175
 Gln Lys Ser Asp Gln Gly Val Glu Gly Pro Gly Gly Thr Gly Gly Ser
 180 185 190
 Gly Ser Ser Val Ser Val Gly Val Asn Pro Leu Ser Phe Val Met Gly

	195		200		205											
Val	Gly	Gly	Gly	Ser	Leu	Gly	Leu	Phe	Tyr	Ile	Pro	Ser	Pro	Ser	Phe	
	210				215				220							
Pro	Leu	Ile	Ile	Thr	Phe	Leu	Thr	Leu	Leu	Gly	Thr	Gly	Gly	Ala	Ala	Lys
225					230				235						240	
Gln	Gly	Leu	Ser	Asn	Ile											
					245											